

National Population Growth Rate, Its Components, and Subnational Contributions: A Research Note

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ABSTRACT A population's current growth rate is determined jointly by changes in fertility, mortality, and migration. This overall growth rate is also the average of age-specific growth rates, which can be decomposed into the result of historical changes in fertility, mortality, and migration. However, doing so requires more than 100 years of historical data, meaning that such analyses are possible only in a select few populations. In this research note, we propose an adapted version of the variable-*r* model to measure contributions to the population growth rate for countries with shorter demographic series. In addition, we extend this model to explore the contribution of subnational changes to the national population growth rate. Our results demonstrate that the age-specific growth rates obtained from short historical series, say 25 years, closely match those of the longer series. These abbreviated age-specific growth rates closely resemble the growth rate at birth of their respective cohorts, which is the major determinant of population growth, except at older ages where mortality becomes the main explanatory element. Exploring subnational populations, we find considerable heterogeneity in the age profile of the components of growth and find that the most populous regions tend to have an outsized impact on national-level growth.

KEYWORDS Variable-*r* • Population growth • Subnational

Introduction

Population growth (increases and declines) remains one of the key demographic concerns worldwide. The world's population will continue growing from 8 billion today to a peak of nearly 10.4 billion around 2080 (United Nations 2022). The simple and elegant demographic balance equation allows researchers to estimate the combined contribution of births, deaths, and migration to these changes in population (Preston et al. 2001). The components of the balance equation can be seen as a prospective perspective of population growth. However, counts of deaths and births are predetermined by the population's composition—for example, aging populations experience a high number of deaths and few births. Alternatively, a retrospective view toward population growth explains current rates of growth as the result of historical demographic events that have shaped the present population composition. This research note builds on previous efforts to disaggregate the demographic history of current

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population growth by Canudas-Romo et al. (2022); we extend this method to shorter time series and disaggregate to subnational populations.

The current population growth rate is the average of the age-specific growth rates, weighted by the population composition (Horiuchi 1991). Those age-specific growth rates are in turn determined by the contribution of historical changes in fertility, mortality, and migration. The variable-*r* model separates the past contribution of each of these demographic components from the age-specific growth rates (Arthur and Vaupel 1984; Lee and Zhou 2017; Murphy 2017; Preston and Coale 1982; Preston and Stokes 2012; Preston and Vierboom 2021). However, traditional variable-*r* methods require extremely long demographic series (birth, mortality, and migration) to explore growth at all ages, with particularly high data demands at oldest-old ages. Using an alternative variable-*r* approach, it is possible to accommodate shorter demographic series and explore the historical demographic contribution between two given years (Canudas-Romo et al. 2021). In this research note, we adapt this approach to the population growth rate. Thus, we derive a direct disaggregation of the age-specific population growth rates that produced today's population into the population growth at an earlier age and the historical cohort survival and migration between the two ages.

Historical trends in fertility, mortality, and migration vary across countries, but substantial variability is also observed within countries' subnational populations (Alexander et al. 2017; Bozick 2021; Nisén et al. 2021). As a consequence, considerable heterogeneity can be hidden within national population growth rates, which may overlook diversity in growth patterns within the subnational populations. To further explore how subnational population changes contribute to national-level growth, we propose an extension of the population growth rate to account for the regional/state contributions.

Data

Our analysis uses age- and sex-specific population counts and death rates for national populations from the Human Mortality Database (HMD), and subnational population data (departments/prefectures/provinces/states/territories) from the available sub-national mortality databases: Australian (AHMD; 2024), Canadian (CHMD; 2024), French (FHMD; 2024), Japanese (JMD; 2024), and the United States Mortality Databases (USMDB; 2024). These databases use the same methods protocol from the HMD, meaning that similar derivations of life table measures are performed for all populations, allowing comparability across countries and subpopulations. The use of this HMD protocol was the main criteria for selecting these countries, which represent a combination of growing and declining (Japan) populations during the studied period. The current HMD methods protocol (version 6) is a result of several iterations experienced during the development of the database. Similar scrutiny and possible subnational-specific methodology will need to be developed for these subnational databases. This is particularly critical for the assumptions on migration that could create bias in results on person-years and, thus, life table measures. Additionally, the information from the countries comprising the United Kingdom (England, Wales, Northern Ireland, and Scotland) from the HMD was also included in our subnational

study. Population counts were obtained from these databases; 2010 to 2020 was the most recent time available across all subnational and national populations and was selected as our time range of analysis. The details of the available information for each of the subnational databases are included in Table A1 in Appendix 1 of the supplementary online materials.

Methods

The population growth rate at time t , or $r(t)$, is the average of the age-specific growth rates weighted by the population composition at each age as

$$r(t) = \int_0^{\omega} r_x(t) c_x(t) dx, \quad (1)$$

where $r_x(t)$ and $c_x(t)$ correspond to the growth rate and population composition at age x and time t , respectively.

To decompose the population growth between two points in time, we apply an extension of the variable- r method (Canudas-Romo et al. 2021). In this truncated variable- r decomposition, the population growth rate at age x and time t , $r_x(t)$, for each cohort is separated into the growth at an earlier age y , or $r_y(t-x+y)$, and the cohort survival and net migration changes between the two ages as

$$r_x(t) = r_y(t-x+y) + \Delta S^{t-x}(y,x) + \Delta M^{t-x}(y,x), \quad (2)$$

where $\Delta S^{t-x}(y,x)$ and $\Delta M^{t-x}(y,x)$ are the changes in cohort survival probabilities and net migration probabilities from a younger age y to the older age x . The change in net migration $\Delta M^{t-x}(y,x)$ is estimated from the residuals of Eq. (2) as in previous studies (Preston and Stokes 2012; Preston and Vierboom 2021). Since our aim is to decompose the population growth between two periods, the age-specific growth rates $r_x(t)$ were calculated from ages 0 to 100. Thus, Eqs. (1) and (2) combine to produce the contribution of growth at an earlier age (referred to as r -past), survival, and net migration to the total population growth.

Equation (1) can also be applied to calculate subnational growth rates, or $r_i(t)$ for subnational population i , defined as $r_i(t) = \int_0^{\omega} r_{x,i}(t) c_{x,i}(t) dx$, where $c_{x,i}(t) = \frac{N_{x,i}(t)}{N_i(t)}$ is the population composition at age x and time t in the subnational population i . To study the contribution of each subnational population i growth rate to the national population growth, there is another average, $r(t) = \sum_i r_i(t) c_i(t)$, where $c_i(t) = \frac{N_i(t)}{N(t)}$ corresponds to population composition at time t in subnational population i with respect to the total population. With substitution, we can derive the formula

$$r(t) = \sum_i \int_0^{\omega} r_{x,i}(t) c_{x,i}(t) c_i(t) dx, \quad (3)$$

where $r_{x,i}(t)$ can be separated with Eq. (2) further into the contribution of survival and net migration as well as the previous growth rate. Additional details of these equations and their derivations are found in online Appendix 2. All calculations were conducted

using R software (R Core Team 2023), and the R codes of the programs used in the analysis are in the GitHub repository (<https://github.com/tyaSHEN/subnational>).

Results

We demonstrate that the growth rate decomposition introduced in Canudas-Romo et al. (2022) can be generalized and applied to shorter time series and subnational populations. We show results decomposing the rate of population growth between 2010 and 2020 for the six selected countries (Australia, Canada, France, Japan, the United Kingdom, and the United States) and their subnational populations. This rate of growth is separated into three terms: the portion resulting from changes in cohort survival probabilities, the portion resulting from changes in cohort net migration probabilities, and the portion resulting from the growth rate at an earlier age (r -past). We test several different time periods of historical information to understand how sensitive our substantive results are to differing time horizons (25, 50, 75, and 100 years). Finally, we explore the drivers of changes in subnational growth rates, focusing on understanding the contribution of the subnational growth rate components to population changes at the national level.

Figure 1 depicts the age contribution to the growth rate from Eq. (1) for the selected countries. The peaks and valleys in the age trends coincide in all nations: high values at ages 5–10, 25–35, and 55–75, and low values at ages 12–25, 40–50, and after age 75. These growth rate contributions correspond to these countries' generation X (or "echo-boomers," aged 25–35), the "baby bust" cohorts (aged 40–50), and the baby boomers between ages 55 and 70. It is worth noting that these age patterns are not universal: fluctuations in the growth rate contributions in Japan are the opposite of the age-specific trends in other countries, excepting the high growth rate above age 70 (Figure A2 in online Appendix 3 includes Japan).

The cross-sectional representation of the population change between 2010 and 2020 shown in Figure 1 can be further decomposed into its historical components as presented in Eq. (2). Figure 2 demonstrates this decomposition by focusing on the U.S. female population growth rate between 2010 and 2020, based on four different periods of historical information: 25, 50, 75, and 100 years. Each panel in Figure 2 includes the age patterns of the components of the age-specific growth rates, namely, the product of the population composition, or $c_v(t)$, with each component: changes in cohort survival probabilities and cohort net migration probabilities, as well as the growth rate at an earlier age (r -past) as described in Eq. (2) and further explained in online Appendix 2. In comparing across these four periods, we find a remarkable similarity between the age contributions. This suggests that short lengths of time are sufficient to estimate the age contributions of survival, net migration, and past growth to the overall growth rate. The consistency in age-specific growth rates over age for any given cohort, except at old ages, is the main reason for the similarity in age contributions. A cohort's growth rate starts at a level set by the growth rate at birth and, although it changes at subsequent ages owing to survival and migration, it remains similar to this initial growth. This similarity between age-specific growth rates and their corresponding growth rate at birth allows us to use shorter series of 25–50 years and still obtain similar age patterns describing the cohorts' demographic history.

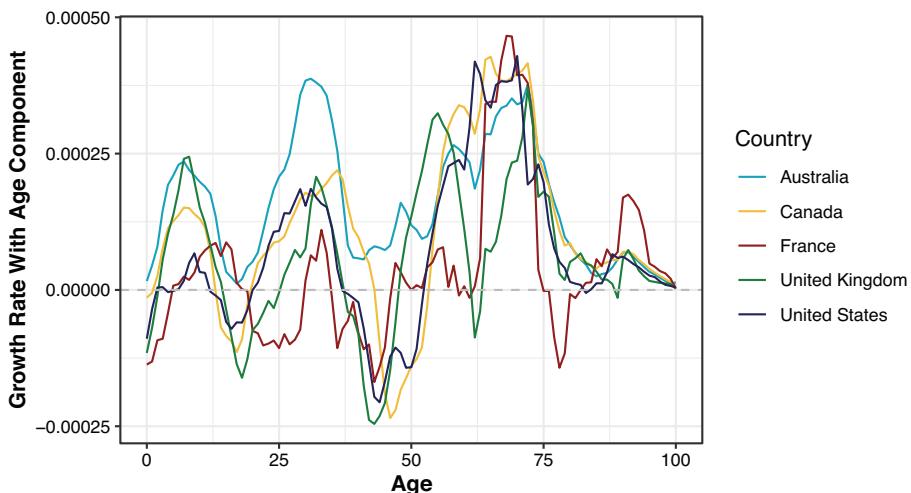


Fig. 1 Age contribution to the female population growth rate between 2010 and 2020, $r_x(t) c_x(t)$, for selected countries. Source: Authors' calculations based on HMD (2024) data.

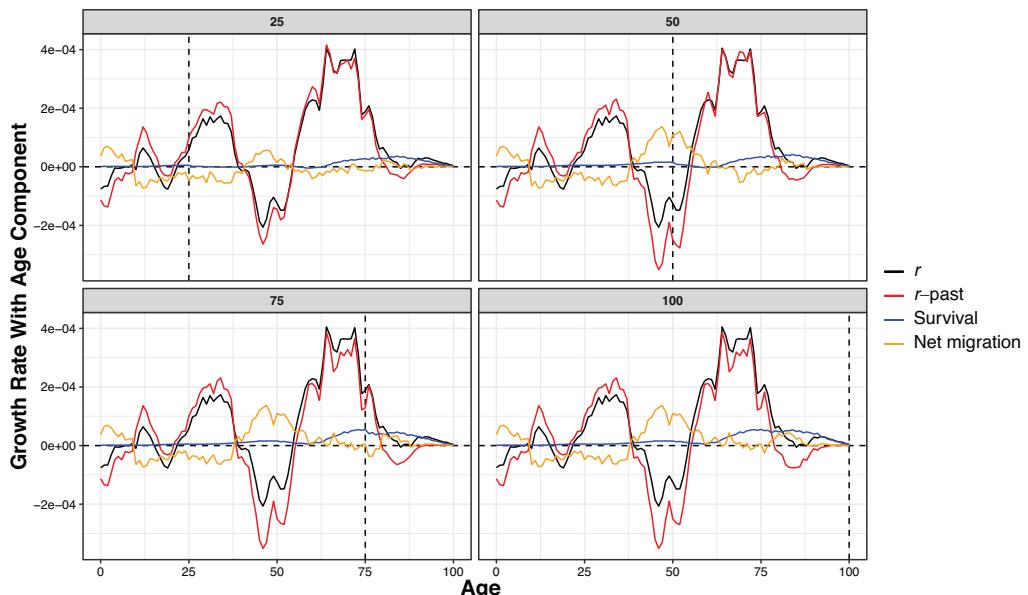


Fig. 2 U.S. female age-specific growth rates between 2010 and 2020, $r_x(t) c_x(t)$, and their components in Eq. (2) with 25, 50, 75, and 100 years of historical data: Age-specific growth rate at a younger age y , or r -past, cohort survival change, and cohort net migration change between ages y and x . The vertical dashed line separates the young ages to the left as those with full cohort historical information and those on the right without that information (see online Appendix 2 for more details). Scientific notation is used on the vertical axis to highlight the small numbers (Burch 2022). Source: Authors' calculations based on data described in online Table A1.

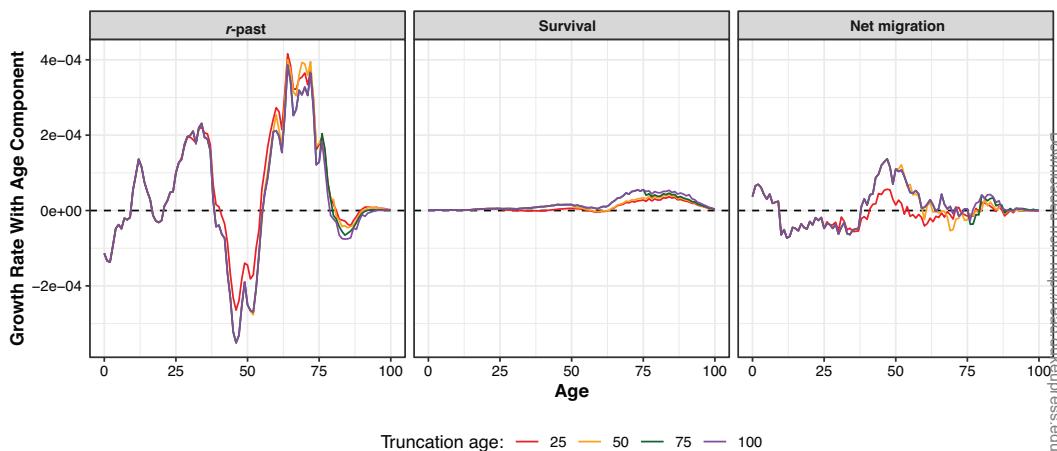


Fig. 3 Components of the U.S. female age-specific growth rates between 2010 and 2020, as in Eq. (2), with 25, 50, 75, and 100 years of historical data: Age-specific growth rate at a younger age y , or r -past, cohort survival change, and cohort net migration change between ages y and x . *Source:* Authors' calculations based on data described in online Table A1.

Although deviations arise between the age-specific growth rates at older ages and their growth rate at birth, these differences play a minor role in the overall growth rate given that they are weighted by the structure of the population. Older adults represent a smaller proportion of the total population, meaning that the contribution of those aged 85 or older to overall growth is small. This is the case even when age-specific growth rates are the highest at older ages (e.g., the highest growth rates for U.S. females between 2010 and 2020 are found at ages 70 and 96; see unweighted Figure A3 in online Appendix 3). At these advanced ages, growth is primarily driven by increases in survival. The contributions to growth vary substantially across cohorts in the United States, ranging from the high growth of baby boomers (aged 55–75) and the “echo-boomers” (aged 25–35) to the low growth rates of the “baby bust” between ages 40 and 50.

Figure 3 further extends the observations of Figure 2 by comparing the components of the growth rate based on 25, 50, 75, or 100 years of historical data. The similarity in growth rate at an earlier age, r -past, is confirmed regardless of the length of the historical series (similar figures are included in online Appendix 3 for the other five countries in this study). However, small errors at each age accumulate and can result in deviations in aggregate results. Table A2 (in online Appendix 3) shows that using shorter time series of historical information leads to the r -past term increasing in explanatory power, while using longer time series leads to an increase in the importance of survival and net migration to the overall growth rate. Thus, there are clear gains in precision by having a longer time series of information, particularly at the age-aggregated level. In other words, using a shorter demographic history leads to more information being contained in the r -past term, while using a longer time series sees this information distributed among the other two components. This is the case even when small deviations are observed at the age-specific level of the components of population growth.

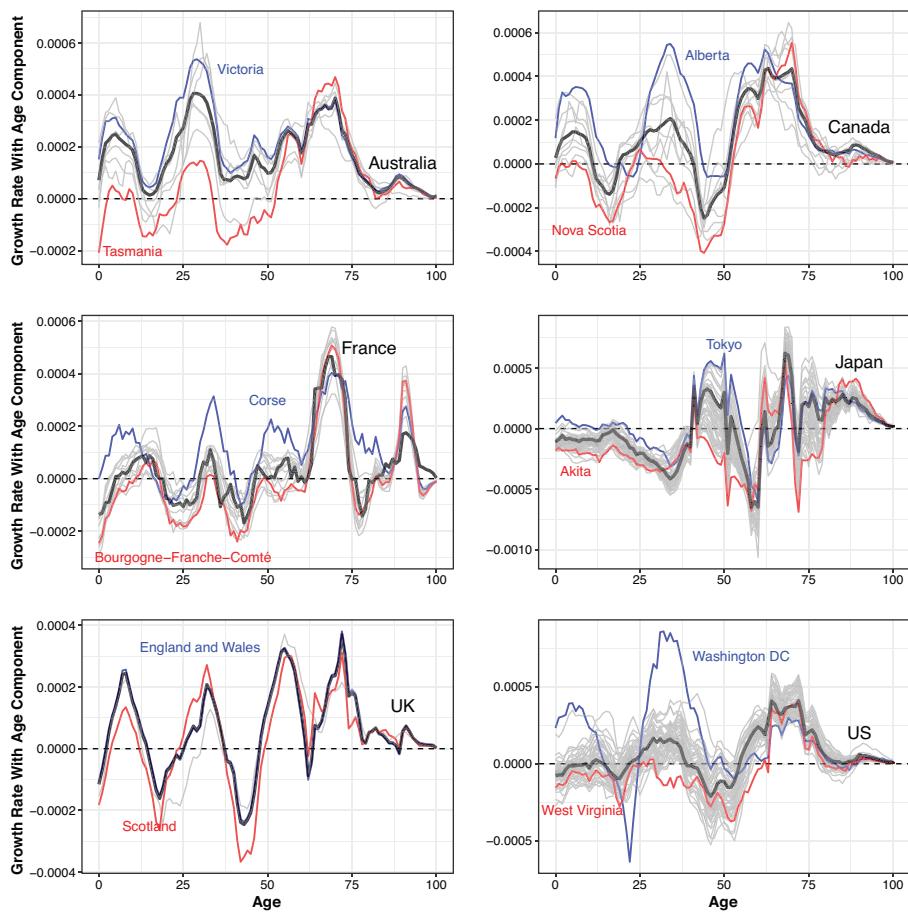


Fig. 4 National and subnational female age-specific growth rates (multiplied by population composition) for selected HMD countries. The subnational populations with the highest and lowest subnational overall growth rates are highlighted for 2010–2020. For the United Kingdom, England and Wales encompass 89% of the population, so this subpopulation and the national age-specific growth rates have practically the same age pattern. *Source:* Authors' calculations based on data described in online Table A1.

Figure 4 presents the national and subnational age-specific growth rates for the selected countries. Also highlighted are the subnational populations with the highest and lowest overall growth rates ($r_i(t) = \int_0^t r_{x,i}(t)c_{x,i}(t)dx$). All subnational populations' age-specific growth rates follow the same age pattern as the national trend, except for Washington, D.C., which has higher growth at young ages (0–5 and 25–35) than the rest of the nation. As expected, the subnational populations with the highest overall growth rates (r_i) also correspond with the highest values of age-specific growth rates. Opposing that are the subpopulations with the lowest growth rates, which also have low age-specific values. For the United Kingdom, England and Wales correspond to 89% of the population, so this subpopulation and the national age-specific growth rates have practically the same age pattern.

Figure 5 shows the age contribution of the components of U.S. population growth between 2010 and 2020, as well as the contribution to this growth from California,

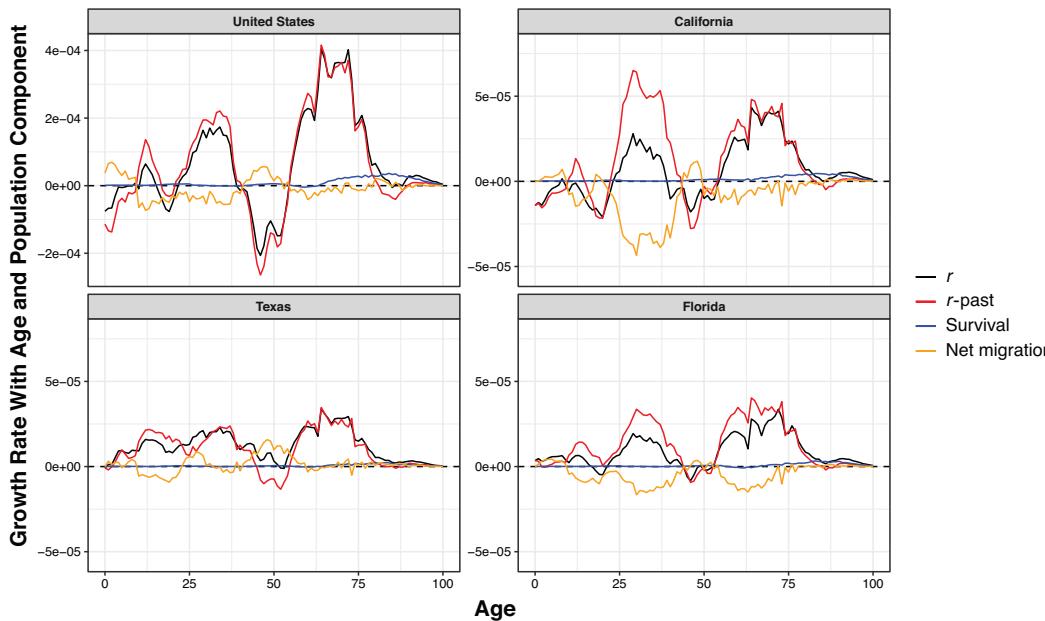


Fig. 5 U.S. female age-specific growth rates between 2010 and 2020, based on 25 years of historical information on survival, net migration, and past growth rate (r -past) as in Eq. (2), and the contribution to those components by the most populous states as in Eq. (3): California, Florida, and Texas. The national vertical axis scale is different than that for the states, since for the state results there is the additional product with the state composition in the nation, the $c_i(t)$ term in Eq. (3). *Source:* Authors' calculations based on data described in online Table A1.

Florida, and Texas. These are the most populous states in the nation, representing 12%, 6%, and 8% of the total population, respectively, and corresponding to the $c_i(t)$ term in Eq. (3). While for the nation the observed values are the product of the population composition, or $c_x(t)$, with each component, for the state results there is the additional product with the state composition in the nation, the $c_i(t)$ term in Eq. (3). Hence, the national growth is dominated by the populous states and age groups, as seen in Figure 4 for the UK. The same scale (vertical axis) is used for the age components for the three states, and although these differ from the national-level results in scale, the age patterns are similar. California and Florida closely follow the trends in age-specific growth of the national level described in Figure 2, with the waves of baby boomers and their echo cohorts present. However, at ages 20–40 the growth rate of the past (r -past) exceeds the growth rate of 2010 to 2020, resulting from negative net migration at these ages. Patterns in Texas are less pronounced than for the other states—at younger ages (the late teens and early 20s), growth is positive, as opposed to the negative age-specific growth observed in the other states and the nation.

The analysis at the subnational level in Figure 5 is extended in Table 1 to include the populations from Australia, Canada, France, Japan, the UK and the United States. The three most populous subnational populations in each country and their contribution to the nation's growth rate between 2010 and 2020 are also included in the table. The contribution to the national growth of each of the subnational populations

Table 1 Female population growth rate between 2010 and 2020 for selected countries, based on historical information on survival, net migration, and past growth rate of 25 years as in Eq. (2), and the contribution of those components of the most populous subnational populations as in Eq. (3)

Country/State	Population (%)	Growth (%)	r-Past	Survival	Net Migration
Australia	100	15.93	9.82	1.15	4.95
New South Wales	32	4.38 (27)	2.45	0.40	1.53
Victoria	25	5.23 (33)	1.68	0.31	3.24
Queensland	20	3.45 (22)	3.79	0.21	-0.55
Sum	78	13.06 (82)	7.92	0.92	4.22
Canada	100	10.85	6.40	1.04	3.40
Ontario	39	4.28 (39)	3.77	0.45	0.05
Quebec	23	1.66 (15)	0.54	0.27	0.85
British Columbia	13	1.98 (18)	2.00	0.15	-0.16
Sum	75	7.92 (73)	6.31	0.87	0.74
United States	100	6.50	6.37	0.89	-0.75
California	12	0.54 (8)	1.08	0.12	-0.66
Texas	8	1.44 (22)	1.21	0.06	0.16
Florida	6	1.37 (21)	1.95	0.11	-0.69
Sum	27	3.35 (51)	4.24	0.29	-1.19
United Kingdom	100	6.22	1.52	1.63	3.09
England and Wales	89	5.80 (93)	1.71	1.44	2.65
Scotland	8	0.29 (5)	-0.24	0.14	0.38
Northern Ireland	3	0.13 (2)	0.07	0.04	0.02
Sum	100	6.22 (100)	1.54	1.62	3.05
France	100	3.80	1.86	1.29	0.65
Île-de-France	19	0.82 (22)	0.63	0.21	-0.02
Auvergne-Rhône-Alpes	12	0.77 (20)	0.41	0.16	0.20
Nouvelle-Aquitaine	9	0.04 (1)	-0.12	0.13	0.03
Sum	40	1.63 (43)	0.92	0.50	0.21
Japan	100	-1.92	-3.84	1.49	0.44
Tokyo	10	0.63 (-33)	-0.87	0.15	1.36
Osaka Prefecture	7	0.00 (0)	-0.40	0.11	0.29
Kanagawa Prefecture	7	0.17 (-9)	0.16	0.09	-0.08
Sum	24	0.80 (-42)	-1.11	0.35	1.57

Notes: Values in columns 2 to 5 have been multiplied by 1,000. Countries are ordered by national growth rate from the highest (Australia, 15.93%) to the lowest (Japan, -1.92%). The percentages of subnational population and contribution to national growth rate are presented in the first and second columns, the latter in parentheses. The UK values do not include the overseas territories, which explains the remaining gaps to the total.

Source: Authors' calculations based on data described in Table A1 in the online supplement.

depends substantially on the proportion of the population in those populations. For example, England and Wales, which correspond to 89% of the population in the UK, explain 93% of their nation population growth of $r=6.22\%$. Similarly, in Australia and Canada, the three major states encompass more than 75% of the population of the country and explain 82% and 73% of their population growth, respectively. In Japan and the United States, the three most populous states correspond to approximately a quarter of the population. However, while for the United States they explain 51% of the population growth, in Japan they are among the few prefectures experiencing population expansion, while at the national level the population size is declining. In

most countries the r -past component is the dominant component, excepting in the UK, where cohort survival is the primary driver of change. The only uniform trend within each country is that of survival, which consistently contributes to increased growth, while r -past and net migration differ both with respect to the national trend and between subnational populations.

Discussion

The national population growth rate, as a single demographic measure, hides the historical demographic contribution of the components of change: fertility, mortality, and migration (Canudas-Romo et al. 2022). In this research note, we integrate the past contribution of these factors to overall population change, even for populations that do not have long demographic series of information. This is possible because age-specific growth rates are very similar to the growth rate at birth of their corresponding cohort (Preston and Vierboom 2021), except at older ages. We find consistency in age-specific trends of the components of the population growth, irrespective of the number of years of observation in all analyzed countries. In other words, at young ages the mortality and migration effects have not disrupted the age-specific growth rates enough for them to differ substantially from their initial growth rate at birth. Nevertheless, excess cohort mortality or migration can cause this trend to be disrupted. For example, in every single population at older ages, the accumulation of mortality improvements in successive cohorts disrupts the similarity between growth rates at old ages and their corresponding growth rate at birth (see online Appendix 3). However, this disparity between growth rates (at old ages and birth) makes only a minor contribution to the national population growth rate, as these advanced ages comprise a small proportion of the total population.

Our proposed extension to the variable- r model has both strengths and weaknesses. First, this variable- r extension can be widely applied to countries irrespective of the length of their available historical demographic data. However, the current model requires country-specific assessment for deciding when there is enough data to apply it, as opposed to having a rule of thumb for all populations. Second, the current model calculations ensure that the elements of the variable- r decomposition sum to the total growth rate. However, this means that the net migration factor, national and international, is calculated as the residual of the other available information (population, births, and deaths). Although this issue arises largely from a lack of high-quality data input on migration, the variable- r extension results can be influenced by this lack of information, particularly in subnational populations. Third, subnational data can return surprising results, such as the growth rates for the largest prefectures in Japan opposing the national trend, mainly as a result of the country's internal migration. However, in most cases, this is unusual and the national results are largely determined by those subnational areas with the biggest population share. Finally, an important consideration is that the extended variable- r model can adapt to first-, second-, or third-order divisions of countries, although the findings will also vary by the geographies used.

How changes at the subnational level relate to the national-level demographic change is key to understanding the overall growth rate and other population metrics. These subnational populations experience great variability in growth (Pezzulo

et al. 2017), with substantial implications for national-level trends. In our illustrations, the most populous subnational populations were the drivers of much of the observed growth at the national level, except for Japan, where they worked against the national population decline. The latter result emphasizes the need to study both changes in subnational populations as well as the contribution of those changes to the national population growth. It is particularly relevant to conduct a unifying analysis of the subnational contributions to national-level growth in cases such as Japan, where some subnational populations are growing while others are declining. A second illustration of subnational trends that highlights the usefulness of the variable-*r* methodology is observed for the U.S. state-level age patterns of the growth rate components in Figures 4 and 5. For these states, unusual historical demographic trends that impact current population growth were identified for Washington, D.C. (Figure 4), and Texas (Figure 5), which differed from national and other state trends. These methods could also be used to explore the contribution of nongeographic subnational groups (such as those defined by educational attainment, race and ethnicity, or migration status) to overall population change. Furthermore, other demographic variables, for example, life expectancy or total fertility rate, can benefit from studying changes at the subnational level, which can have differential contributions to national results.

Conclusion

Even as we age, a photograph from the past shows the sustained traits of an individual that exist in the present day. Similarly, a population's age-specific growth rates resemble the levels of their corresponding growth rate at birth and can be used instead of the birth values in variable-*r* applications. Our proposed method develops this relationship, allowing researchers to use shorter periods of historical data and account for subnational contributions when exploring changes to the national growth rate. ■

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References

- Alexander, M., Zagheni, E., & Barbieri, M. (2017). A flexible Bayesian model for estimating subnational mortality. *Demography*, 54, 2025–2041.
- Arthur, W. B., & Vaupel, J. W. (1984). Some general relationships in population dynamics. *Population Index*, 50, 214–226.
- Australian Human Mortality Database*. (2024). Australian National University. Available from demography.cass.anu.edu.au/research/australian-human-mortality-database
- Bozick, R. (2021). Age, period, and cohort effects contributing to the great American migration slowdown. *Demographic Research*, 45, 1269–1296. <https://doi.org/10.4054/DemRes.2021.45.42>
- Burch, T. (2022, January 13). On the use of engineering notation in demography: A technical note. *Demotrends*. Retrieved from demotrends.org/2022/01/13/
- Canadian Human Mortality Database*. (2024). Montréal, Quebec, Canada: Université de Montréal; Rostock, Germany: Max Planck Institute for Demographic Research; Berkeley, CA, USA: University of California, Berkeley. Available from www.bdlc.umontreal.ca/CHMD/index.htm

- Canudas-Romo, V., Shen, T., & Payne, C. (2021). The role of reductions in old-age mortality in old-age population growth. *Demographic Research*, 44, 1073–1084. <https://doi.org/10.4054/DemRes.2021.44.44>
- Canudas-Romo, V., Shen, T., & Payne, C. F. (2022). The components of change in population growth rates. *Demography*, 59, 417–431. <https://doi.org/10.1215/00703370-9765067>
- French Human Mortality Database. (2024). French Regional Database. Paris, France: French Institute for Demographic Studies; Paris School of Economics. Available from frdata.org/fr/french-human-mortality-database/
- Horiuchi, S. (1991). Assessing the effects of mortality reduction on population ageing. *Population Bulletin of the United Nations*, 31–32, 38–51.
- Human Mortality Database. (2024). Rostock, Germany: Max Planck Institute for Demographic Research; Berkeley, CA, USA: University of California, Berkeley; Paris, France: French Institute for Demographic Studies. Available from www.mortality.org
- Japanese Mortality Database. (2024). Tokyo, Japan: National Institute of Population and Social Security Research. Available from www.ipss.go.jp/p-toukei/JMD/index-en.asp
- Lee, R., & Zhou, Y. (2017). Does fertility or mortality drive contemporary population aging? The revisionist view revisited. *Population and Development Review*, 43, 285–301.
- Murphy, M. (2017). Demographic determinants of population aging in Europe since 1850. *Population and Development Review*, 43, 257–283.
- Nisén, J., Klüsener, S., Dahlberg, J., Dommermuth, L., Jasilioniene, A., Kreyenfeld, M., . . . Myrskylä, M. (2021). Educational differences in cohort fertility across sub-national regions in Europe. *European Journal of Population*, 37, 263–295.
- Pezzulo, C., Hornby, G. M., Sorichetta, A., Gaughan, A. E., Linard, C., Bird, T. J., . . . Tatem, A. J. (2017). Sub-national mapping of population pyramids and dependency ratios in Africa and Asia. *Scientific Data*, 4, 170089. <https://doi.org/10.1038/sdata.2017.89>
- Preston, S. H., & Coale, A. J. (1982). Age structure, growth, attrition, and accession: A new synthesis. *Population Index*, 48, 217–259.
- Preston, S. H., Heuveline, P., & Guillot, M. (2001). *Demography: Modelling and measuring population processes*. Oxford, UK: Blackwell.
- Preston, S. H., & Stokes, A. (2012). Sources of population aging in more and less developed countries. *Population and Development Review*, 38, 221–236.
- Preston, S. H., & Vierboom, Y. C. (2021). The changing age distribution of the United States. *Population and Development Review*, 47, 527–539.
- R Core Team. (2023). *R: A language and environment for statistical computing* (Version 4.3.0) [Computer software]. Vienna, Austria: R Foundation for Statistical Computing. Available from <https://www.r-project.org/>
- United Nations. (2022). *World population prospects 2022* (Report). New York, NY: United Nations, Department of Economic and Social Affairs, Population Division. Available from <https://population.un.org/wpp/>
- United States Mortality Database. (2024). Berkeley, CA, USA: University of California, Berkeley. Available from usa.mortality.org

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